

FIGURES

<i>H. pylori</i>	MEMN	N	F F Y	IADRFHVNIGDL VF	F F Q	RDH -DMPS	EI	NHAN-----Y							
<i>D. radiodurans</i>	MPDMAN	D	F F Y	LAGVHTTPEGIO SF	F F Q	AGA -DPAA	GY	DHLE-----C							
<i>H. influenzae</i>	MPL	F	F F A	IAFTMTTPEGIN TV	F F I	FEI -SPFG	GF	DHLN-GDSIE							
<i>C. jejuni</i>	MPL	F	F I A	LAFTMTTPEGID SV	F F I	FDI -SEFG	GF	DHLN-SNSVE							
<i>B. burgdorferi</i>	MKE T	1	F F G	YVS-REFGELAVI TTI	IFA	IEP IENAA	I	G TL NNEV--WTEK Y G							
<i>C. perfringens</i>	MVK	E	F F Y	FAFTMTTPEGII SN	F F Q	FEL -SDFG	GF	EFLL-----E							
<i>N. meningitidis</i>	MPL	F	F F A	VAFTMTTPEGIA TV	F F V	FEI -FEFG	GF	DHLN-GNSVE							
<i>S. typhimurium</i>	MPL	A	F F A	VAFTMTTPEGIA TV	F F I	FEV -FEFG	GF	DHLN-GNSVE							
<i>V. harveyi</i>	MPL	T	F F A	VAFTMTTPEGIT TV	F F A	FEI -SEFG	GF	NHLN-GDSVE							
<i>E. coli</i>	MPL	T	F F A	VAFTMTTPEGIA TV	F F V	FEV -FEFG	GF	NHLN-GNSVE							
<i>V. cholerae</i>	MPL	T	F F A	VAFTMTTPEGIT TV	T F Q	FIL -EPGA	FY	NHLN-GNSVE							
<i>B. subtilis</i>	MPS	E	NA V Y	HGVHENGSTGV NK	F F Q	FQA -FHIT	FT	SHAFYIHFED							
<i>D. radiodurans</i>	MPT	E	I F F	PCVHENGSTGV NK	F F Q	FQA -FHIV	LN	EPAFYIHFED							
Numbering	1	10	20	30	40	50	60	70	80						
Secondary structure	3333		SSSSSSSS	SSSSSSSS	SSSSSSSS		HHHHHHHHHHHHHHHHHH	SSSSSS							
	H1		S1		S2		H2		S3						
<i>H. pylori</i>	Q	T	LNRDNYTE	E	EKT	QIV	FAF---E	ASNEFL	WAAN	T	EG	QNLAPA	DKPAWSEVGV		
<i>D. radiodurans</i>	F	M	A	I	FEDEQG	F	EAA	FIT	GLI-L-P	GVSELE	NYED	D	AA	EQHAFD	DGLFVGETILLER
<i>H. influenzae</i>	F		S	I	TFDEQR	SE	LAS	LDV	AVQIAS	ELNIV	STTE	S	ED	HEIAPN	ASGIGVNFEDLSLNSILF
<i>C. jejuni</i>	F		S	I	TFDEKQ	F	EAA	FDV	AVQDSF	ELNIV	TCAM	S	DE	FLIAPN	NAGISLNNFELMLENA
<i>B. burgdorferi</i>	F		I	F	DYESKD	D	SWL	FEI	MFGE--I	GASDFF	NYFE	N	DM	FRESSE	QIENNIKEENLQYP
<i>C. perfringens</i>	F		TSF	DIIDVQ	E	EYS	FEV	E---QEE	AANEL	SAFL	S	EL	FSHAQ	ENGISQEFYVE	
<i>N. meningitidis</i>	F		S	I	TESELE	D	LAS	LDV	AVQDSF	ELNIV	TCAM	S	AE	FLIAPN	AFHVAVNFNEELTLDEGLLA
<i>S. typhimurium</i>	F		S	I	TFDEQR	D	PZA	ADV	AVQDNG	ELNIV	TCAM	S	SE	FLIAPN	ESQVFNSEFLALPKELQELHI
<i>V. harveyi</i>	F		S	I	TESELE	D	LAA	LDV	AVQDNG	ELNIV	TCAM	S	DE	FLIAPN	EVGVATNFNIELALPESMLFELRID
<i>E. coli</i>	F		S	I	TESELE	D	LAA	LDV	AVQDNG	ELNIV	TCAM	S	DE	FLIAPN	ESQVFNSEFLALPKELQELHI
<i>V. cholerae</i>	F		S	I	AETELE	Q	LAA	LDV	AVQDNG	ELNIV	TCAM	S	DE	FLIAPN	AAGISVNFNIELALPESMLNELKVH
<i>B. subtilis</i>	D		V	S	RFTSAE	D	EDT	FEV	VEIT--E	AANEL	QAFI	I	EG	FLMFP	SQDKELIKVFG
<i>D. radiodurans</i>	D		I	S	RFTVSE	D	EQT	EYS	ELR---E	AANEL	QAFI	I	EG	FLMFP	SHERKSLTKVFES
Numbering	90	100	110	120	130	140	150	160	170						
	SSSSSS	HHHHHHHHHHHHHHHH				HHHHHHHHHHHH									
	S4	H3				d4									

Figure 1 Sequence alignment of LuxS proteins. Color coding: red = greater than 92% identity (or homology in the case of F/Y, S/T, or D/E) and green = hydrophobic residues (A/V/I/L/M/W/Y/F). At the bottom is indicated the residue numbering employed as well as the common secondary structure elements determined in this invention with 3 = 3/10 helix, S = beta strand, and H = alpha helix.

FIG. 2. Represenatative diffraction image from a *H. pylori* LuxS crystal analyzed in this patent.

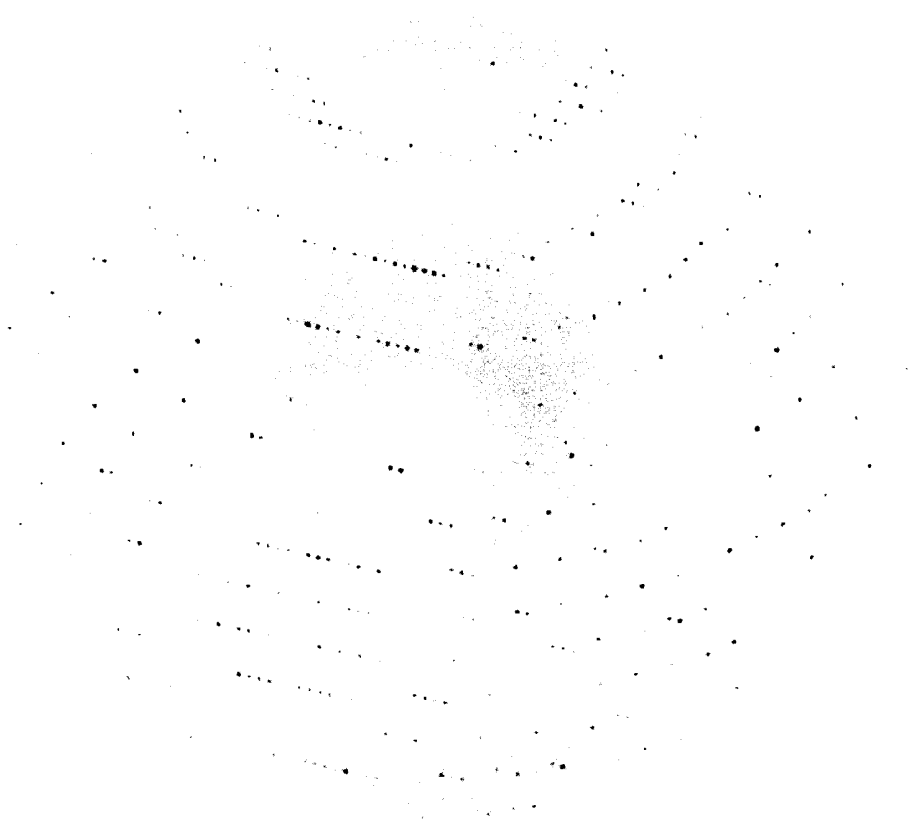


FIG 3. Represenatative diffraction image from a *H.influenzaei* LuxS crystal analyzed in this patent.

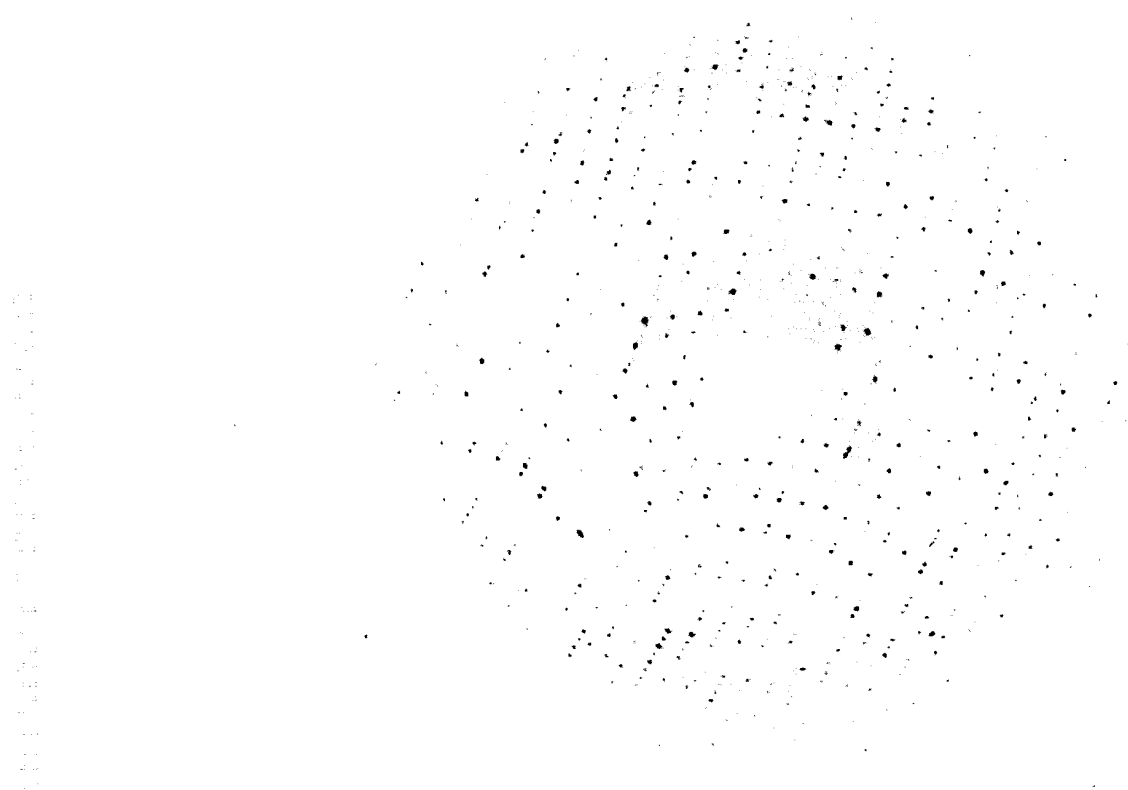


FIG 4. Represenatative diffraction image from $P2_1$ spacegroup *D. radiodurans* LuxS crystals analyzed in this patent.

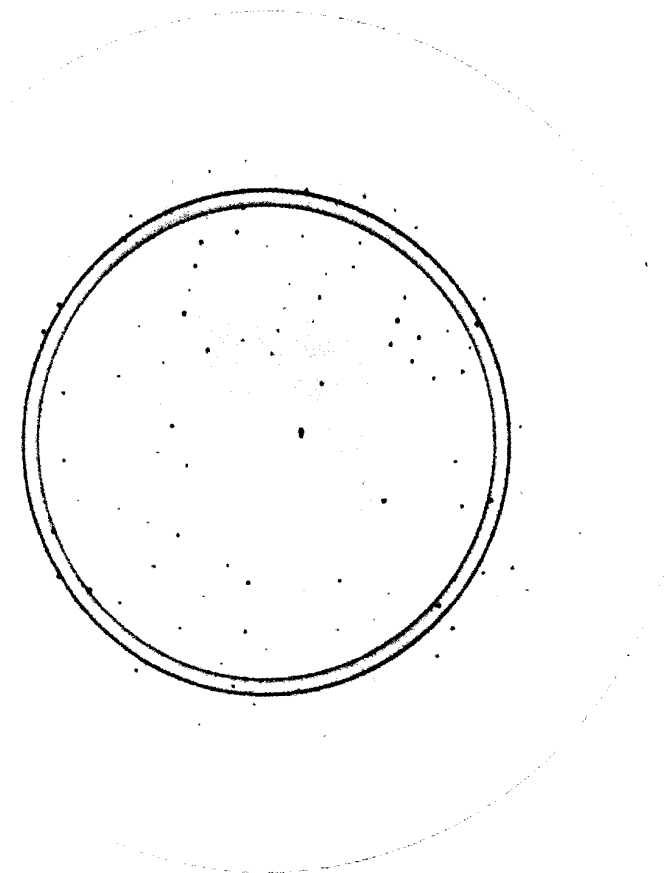


FIG 5. Represenataive diffraction image from C2 spacegroup *D. radiodurans* LuxS crystals analyzed in this patent.

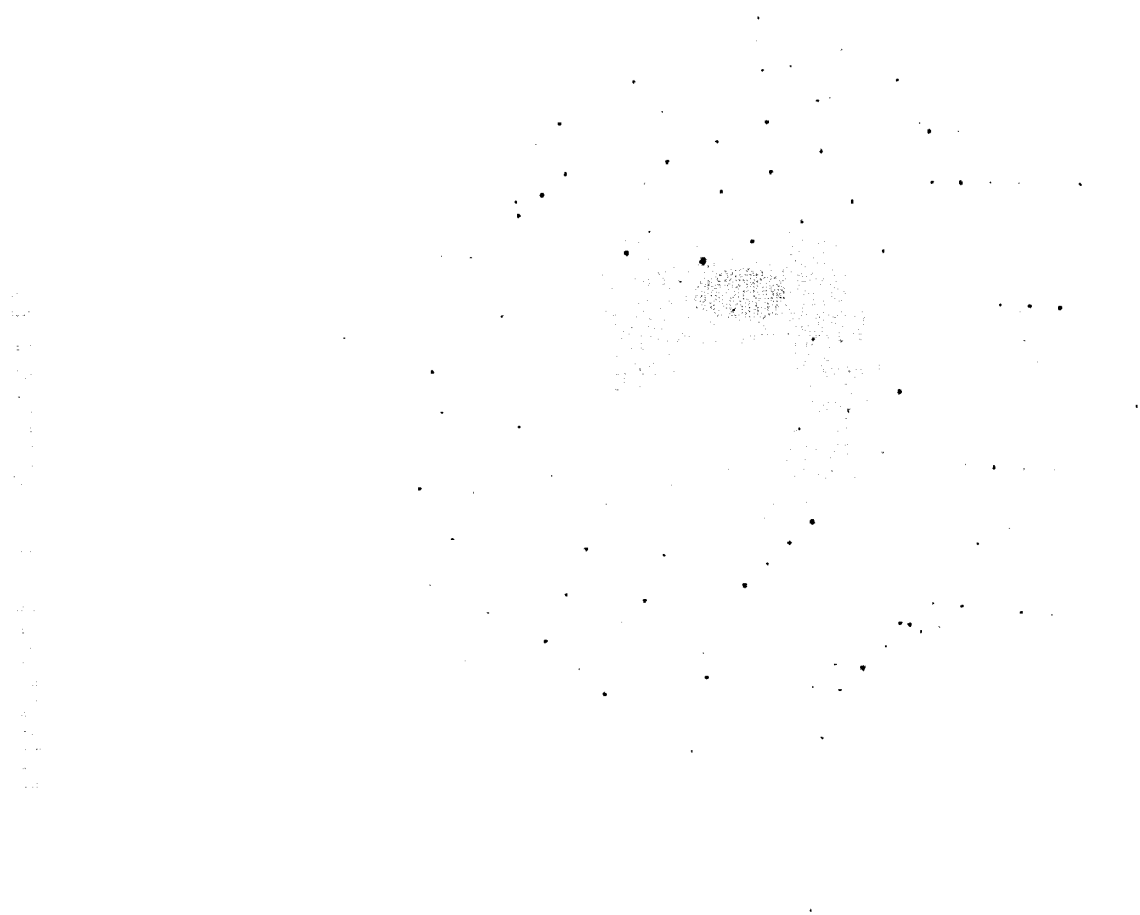


FIG. 6A Ribbon diagrams of the *D. radiodurans* LuxS protein, molecule A.

***D. radiodurans* LuxS (molecule A)**

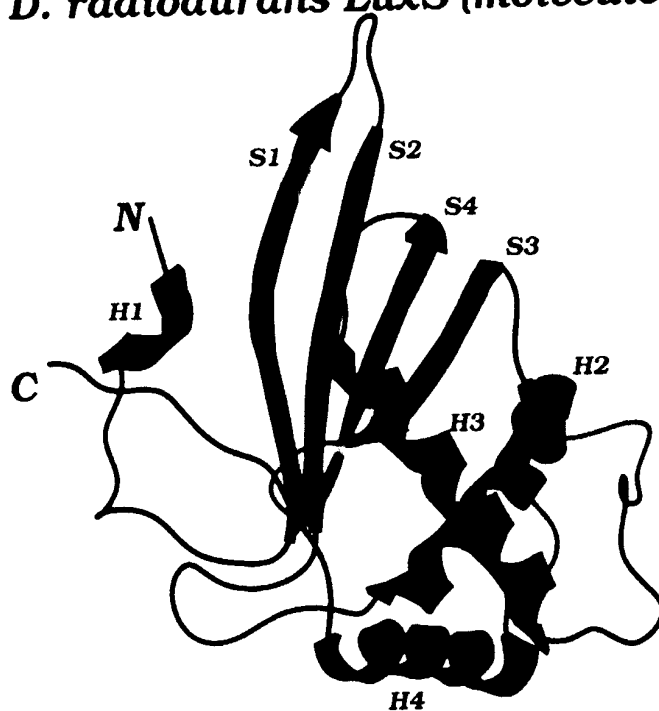
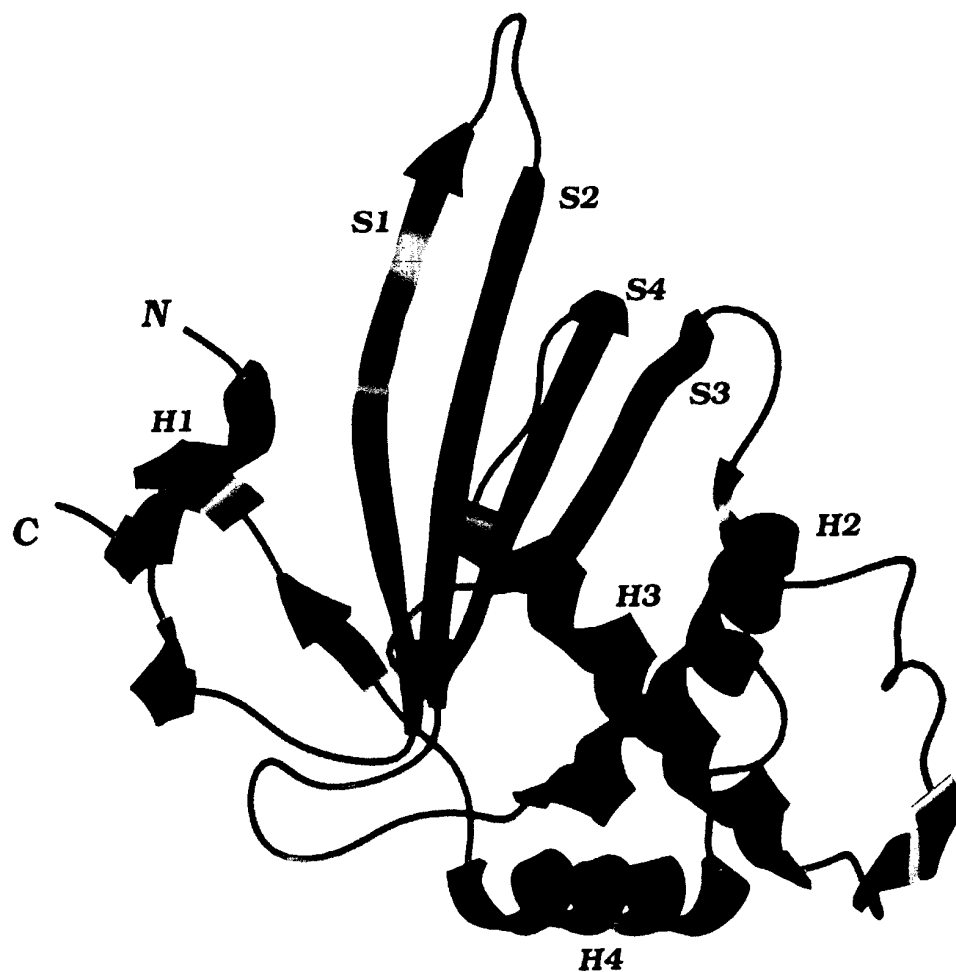
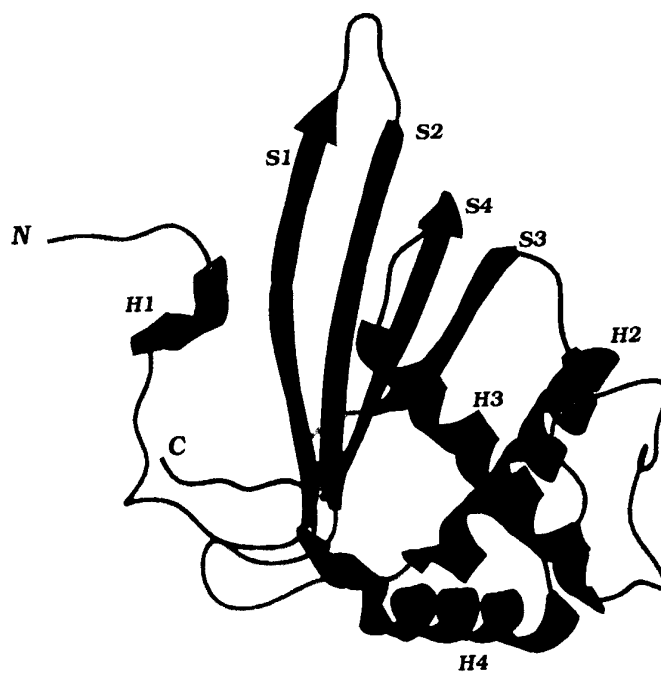


FIG. 6B Ribbon diagrams of the *H. influenzae* LuxS protein, molecule A.



H. influenzae LuxS (molecule A)

FIG. 6C Ribbon diagrams of the *H. pylori* LuxS protein, molecule B.



***H. pylori* LuxS (molecule B)**

FIG. 7A Ribbon diagram of *H. pylori* LuxS as a dimer, the contents of the asymmetric unit.

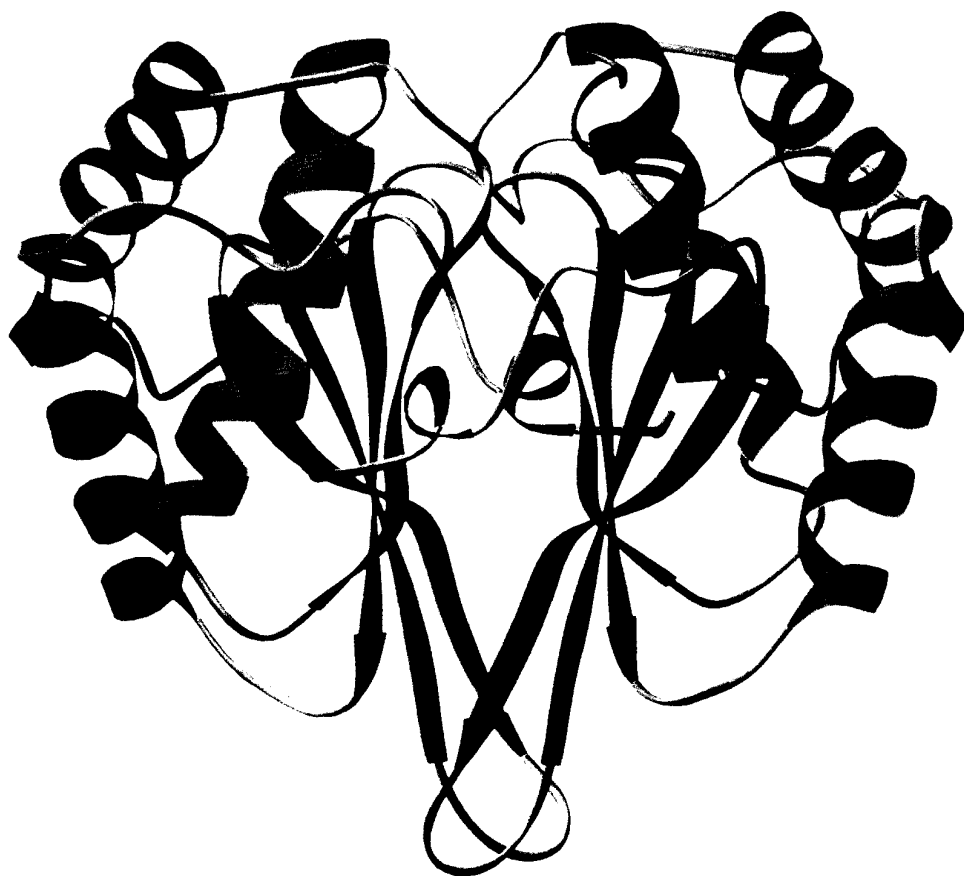


FIG. 7B Ribbon diagram of *H. influenzae* LuxS as a dimer with the bound methionines indicated in ball and stick.

H. influenzae Dimerization



FIG. 8. Stereo image of C-alpha backbone of the *H. pylori* LuxS protein (same orientation as in FIG. 2A)

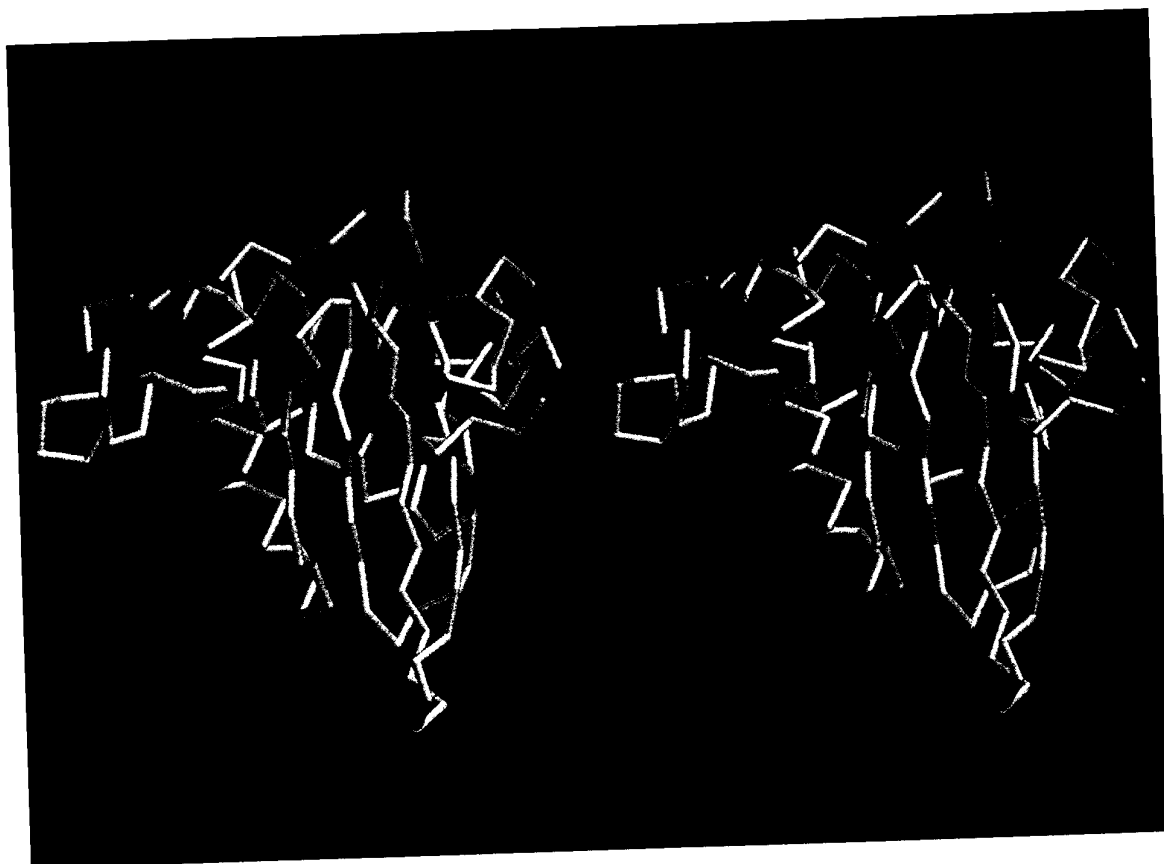


FIG. 9A Region of high sequence variability in LuxS as represented by Helix 3 (see FIG. 1). Helix 3 is the central (diagonal) helix closest to the observer.

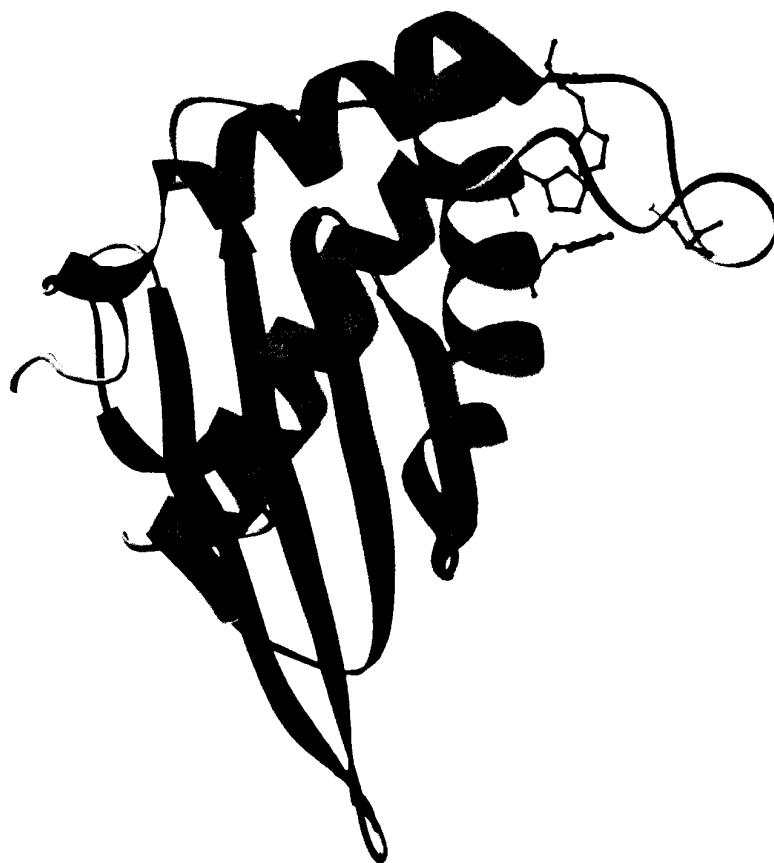


FIG. 9B Region of high sequence conservation in LuxS as represented by Helix 2 (see FIG. 1). Helix 2 is the central (vertical) helix closest to the observer.



FIG. 10A The putative active site of LuxS.



FIG. 10B The active site may enlarge through dimerization of LuxS molecules in vivo, as illustrated by the dimer found in the asymmetric unit of the LuxS crystal.



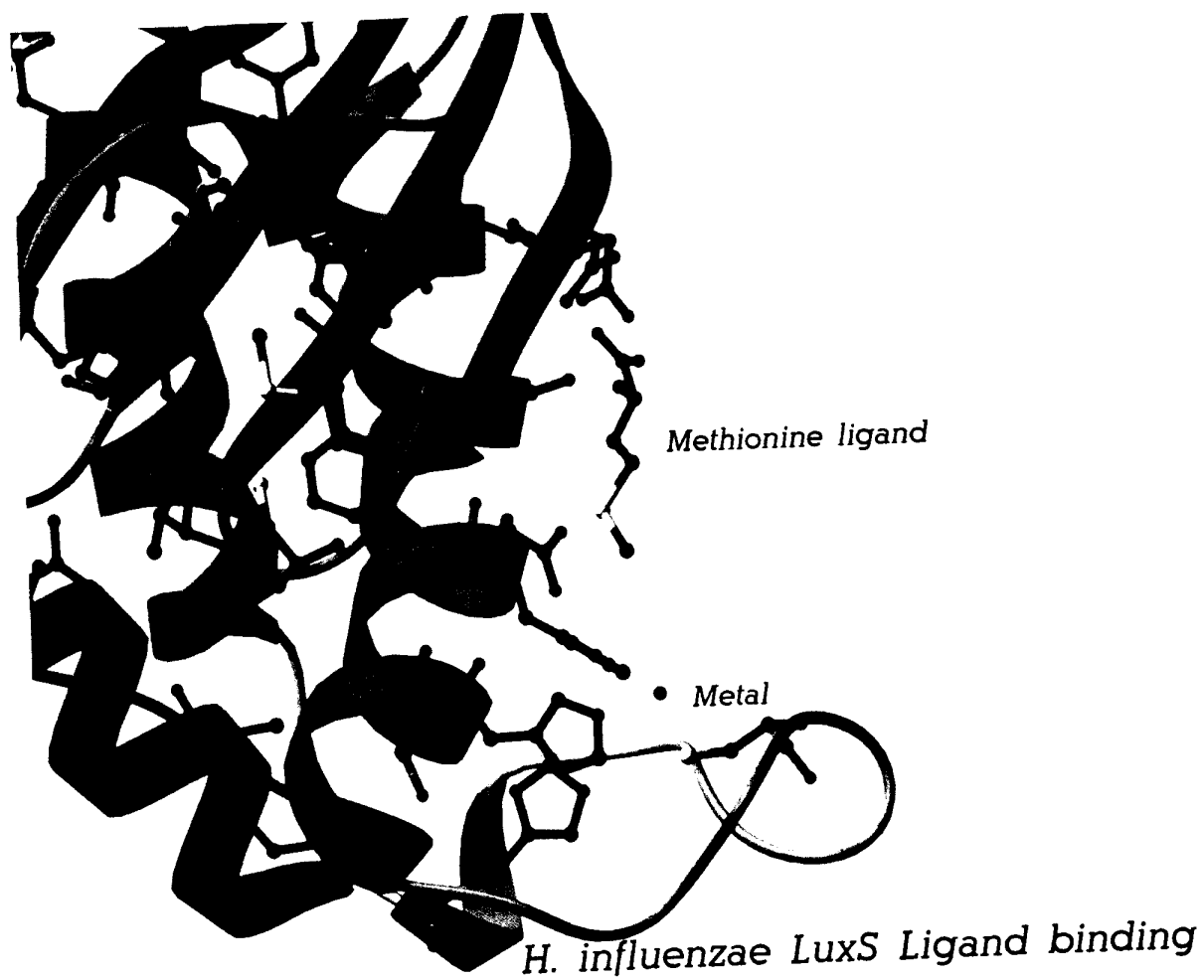


FIG. 11. Proximity of methionine binding site to metal binding site.

H. influenzae LuxS dimerization

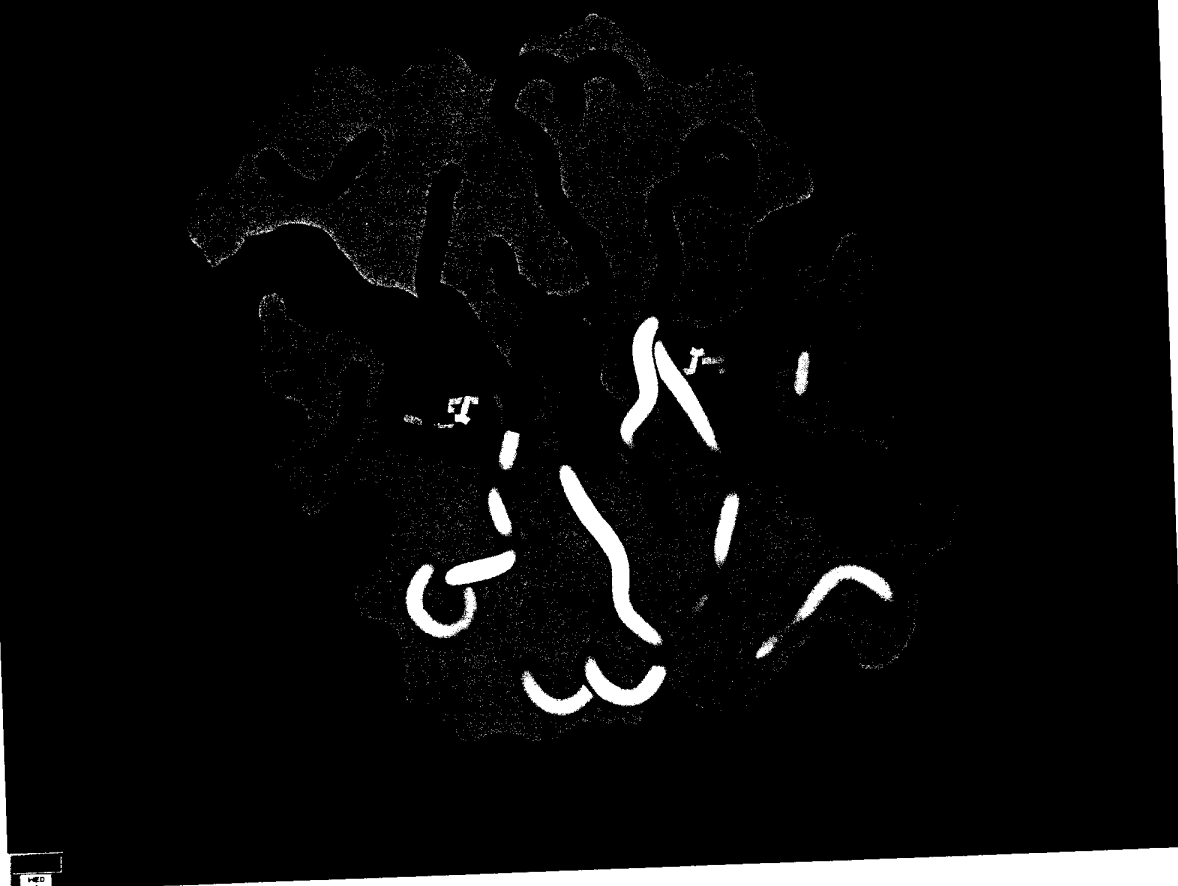


FIG. 12. SPOCK diagram of the molecular surfaces of the two molecule in the asymmetric unit of *H. influenzae* LuxS, cut away partially to reveal binding of the methionine ligands (ball and stick) and a channel through the opposing monomer leading out to the surface. A second channel to the binding site can also be seen. Worms represent the backbone atoms of the proteins in the cut away region.

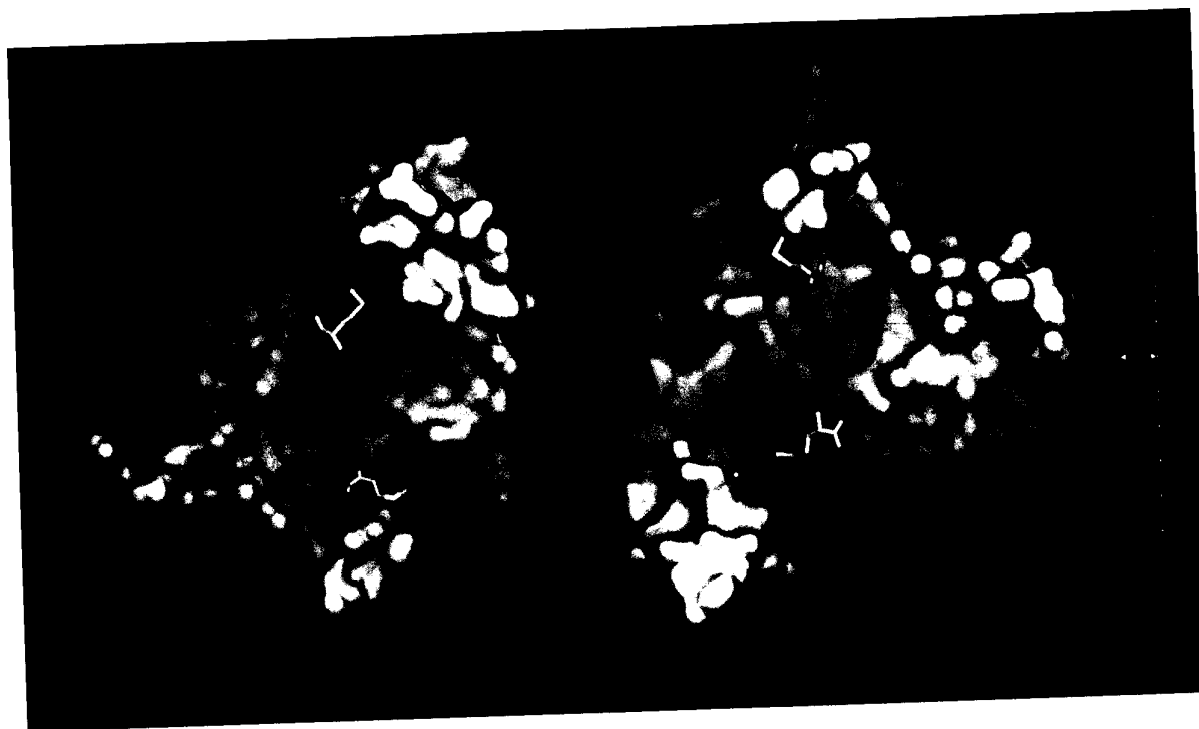


FIG. 13A Molecular surface diagram of the *H. influenzae* LuxS dimer, separated and rotated to the viewer. The methionine ligand are represented as ball and stick, one per monomer with the virtual gold ligands representing where the methionine would lay across the opposing molecule. Red represent negative potential and blue positive potential. The charge complementarity of the dimerization is clear.

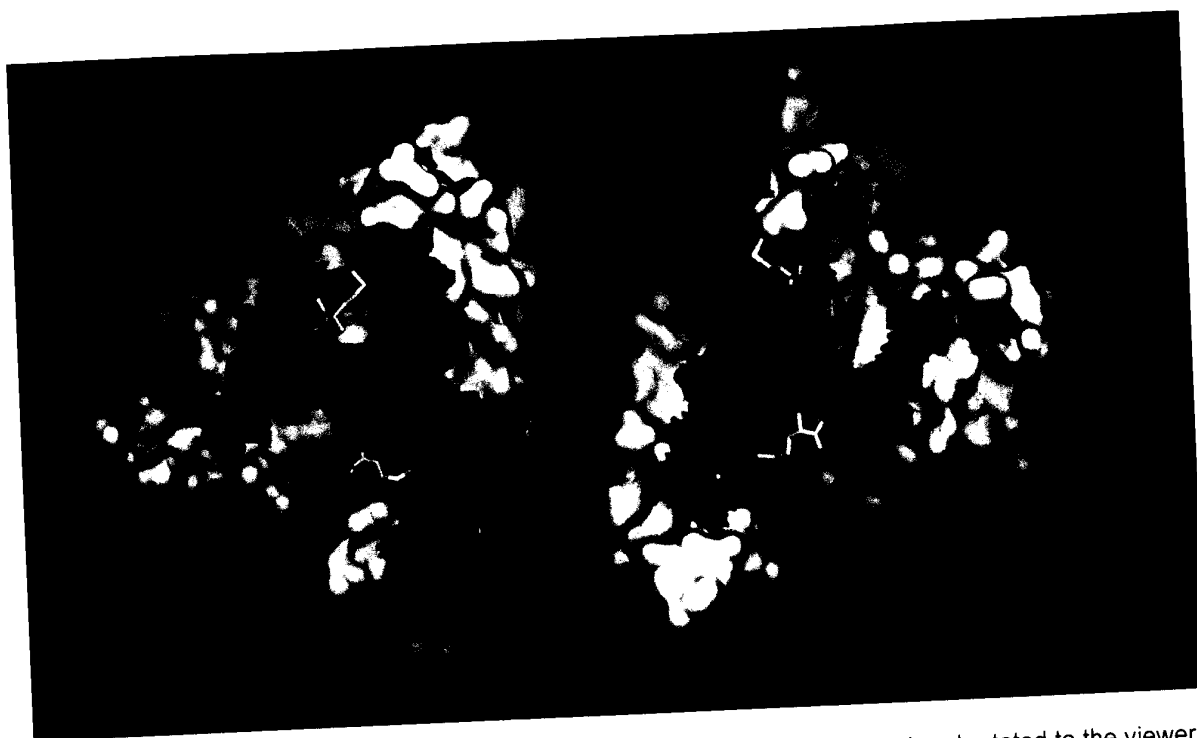


FIG. 13B Molecular surface diagram of the *H. influenzae* LuxS dimer, separated and rotated to the viewer. The methionine ligand are represented as ball and stick, one per monomer with the virtual gold ligands representing where the methionine would lay across the opposing molecule. Green represents conserved hydrophobic residues and red other conserved residues in the LuxS family (same as the color coding in FIG. 1).